#12

SEQUENCE LISTING

<110> Skeiky, Yasir
Reed, Steven
Alderson, Mark
Corixa Corporation

<120> Fusion Proteins of Mycobacterium Tuberculosis

<130> 014058-009070US

<140> US 09/886,349
<141> 2001-06-20

<150> US 09/597,796
<151> 2000-06-20

<150> US 60/265,737
<151> 2001-02-01

<160> 50

<170> PatentIn Ver. 2.1

<210> 1
<211> 1872
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB32A (Ra35FL)

<220>
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cccgtccgcg atggtcgccc aagtggcgcc acaggtggtc aacatcaaca ccaaactggg 300
ctacaacaac gccgtgggcg ccgggaccgg catcgtcatc gatcccaacg gtgtcgtgct 360
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gacattgaac gggttgatcc agttcgatgc cgcaatccag cccggtgatt cgggcgggcc 720
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cttgggtgtt gtcgacaaca acggcaacgg cgcacgagtc caacgcgtgg tcggaagcgc 960
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cagccgtgat tgccgcgtga gcccccgagt tccgtctccc gtgcgcgtgg cattgtggaa 1260
gcaatgaacg aggcagaaca cagcgttgag caccctcccg tgcagggcag ttacgtcgaa 1320
ggcggtgtgg tcgagcatcc ggatgccaag gacttcggca gcgccgccgc cctgcccgcc 1380

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tggcttggca tcgactgcat ctgttgccgc cgttcctacg actcaccgct gcgcgacggc 1560
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aatcacacct cggagtcgca cccctggttt caggagtccc gccgcgaccc agacggaccg 1740
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<210> 2
<211> 355
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB32A (Ra35FL)

<400> 2

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             20                  25                  30

Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
         35                  40                  45

Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
     50                  55                  60

Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65                  70                  75                  80

Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
                 85                  90                  95

Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
            100                 105                 110

Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
        115                 120                 125

Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
    130                 135                 140

Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
145                 150                 155                 160

Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
                165                 170                 175

Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
            180                 185                 190

Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
        195                 200                 205

Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
    210                 215                 220
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```
Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
225                 230                 235                 240

Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
                245                 250                 255

Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
            260                 265                 270

Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
        275                 280                 285

Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
    290                 295                 300

Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
305                 310                 315                 320

Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
                325                 330                 335

Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
            340                 345                 350

Pro Pro Ala
        355
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<210> 3
<211> 1002
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB32A (Ra35 mature)

<400> 3
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ttccccgcgc tgcccctcga cccgtccgcg atggtcgccc aagtggggcc acaggtggtc 120
aacatcaaca ccaaactggg ctacaacaac gccgtgggcg ccgggaccgg catcgtcatc 180
gatcccaacg gtgtcgtgct gaccaacaac cacgtgatcg cgggcgccac cgacatcaat 240
gcgttcagcg tcggctccgg ccaaacctac ggcgtcgatg tggtcgggta tgaccgcacc 300
caggatgtcg cggtgctgca gctgcgcggt gccggtggcc tgccgtcggc ggcgatcggt 360
ggcggcgtcg cggttggtga gcccgtcgtc gcgatgggca acagcggtgg gcagggcgga 420
acgccccgtg cggtgcctgg cagggtggtc gcgctcggcc aaaccgtgca ggcgtcggat 480
tcgctgaccg gtgccgaaga gacattgaac gggttgatcc agttcgatgc cgcgatccag 540
cccggtgagg cgggcgggcc cgtcgtcaac ggcctaggac aggtggtcgg tatgaacacg 600
gccgcgtccg ataacttcca gctgtcccag ggtgggcagg gattcgccat tccgatcggg 660
caggcgatgg cgatcgcggg ccagatccga tcgggtgggg ggtcacccac cgttcatatc 720
gggcctaccg ccttcctcgg cttgggtgtt gtcgacaaca acggcaacgg cgcacgagtc 780
caacgcgtgg tcgggagcgc tccggcggca agtctcggca tctccaccgg cgacgtgatc 840
accgcggtcg acggcgctcc gatcaactcg gccaccgcga tggcggacgc gcttaacggg 900
catcatcccg gtgacgtcat ctcggtgacc tggcaaacca agtcgggcgg cacgcgtaca 960
gggaacgtga cattggccga gggacccccg gcctgagaat tc                    1002
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<210> 4
<211> 330
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB32A (Ra35 mature)

<400> 4

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Met His His His His His His Ala Pro Pro Ala Leu Ser Gln Asp Arg
  1               5                  10                  15

Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala
             20                  25                  30

Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn
         35                  40                  45

Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val
     50                  55                  60

Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala
 65                  70                  75                  80

Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr
                 85                  90                  95

Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly
            100                 105                 110

Leu Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val
        115                 120                 125

Val Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val
    130                 135                 140

Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser
145                 150                 155                 160

Leu Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala
                165                 170                 175

Ala Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly
            180                 185                 190

Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser
        195                 200                 205

Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile
    210                 215                 220

Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile Gly
225                 230                 235                 240

Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly
                245                 250                 255

Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly
            260                 265                 270

Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn
        275                 280                 285

Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp
    290                 295                 300
```

```
Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly
305                 310                 315                 320

Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
                325                 330
```

<210> 5
<211> 1002
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ra35FLMutSA

<400> 5

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aacatcaaca ccaaactggg ctacaacaac gccgtgggcg ccgggaccgg catcgtcatc 180
gatcccaacg gtgtcgtgct gaccaacaac cacgtgatcg cgggcgccac cgacatcaat 240
gcgttcagcg tcggctccgg ccaaacctac ggcgtcgatg tggtcgggta tgaccgcacc 300
caggatgtcg cggtgctgca gctgcgcggt gccggtggcc tgccgtcggc ggcgatcggt 360
ggcggcgtcg cggttggtga gcccgtcgtc gcgatgggca acagcggtgg gcagggcgga 420
acgccccgtg cggtgcctgg cagggtggtc gcgctcggcc aaaccgtgca ggcgtcggat 480
tcgctgaccg gtgccgaaga gacattgaac gggttgatcc agttcgatgc cgcgatccag 540
cccggtgatg cgggcgggcc cgtcgtcaac ggcctaggac aggtggtcgg tatgaacacg 600
gccgcgtccg ataacttcca gctgtcccag ggtgggcagg gattcgccat tccgatcggg 660
caggcgatgg cgatcgcggg ccagatccga tcgggtgggg ggtcacccac cgttcatatc 720
gggcctaccg ccttcctcgg cttgggtgtt gtcgacaaca acggcaacgg cgcacgagtc 780
caacgcgtgg tcgggagcgc tccggcggca agtctcggca tctccaccgg cgacgtgatc 840
accgcggtcg acggcgctcc gatcaactcg gccaccgcga tggcggacgc gcttaacggg 900
catcatcccg gtgacgtcat ctcggtgacc tggcaaacca agtcgggcgg cacgcgtaca 960
gggaacgtga cattggccga gggacccccg gcctgagaat tc                    1002
```

<210> 6
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ra35FLMutSA

<400> 6

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Met His His His His His His Ala Pro Pro Ala Leu Ser Gln Asp Arg
  1               5                  10                  15

Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala
             20                  25                  30

Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn
         35                  40                  45

Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val
     50                  55                  60

Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala
 65                  70                  75                  80

Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr
                 85                  90                  95
```

```
Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly
            100                 105                 110

Leu Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val
        115                 120                 125

Val Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val
    130                 135                 140

Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser
145                 150                 155                 160

Leu Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala
                165                 170                 175

Ala Ile Gln Pro Gly Asp Ala Gly Gly Pro Val Val Asn Gly Leu Gly
            180                 185                 190

Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser
        195                 200                 205

Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile
    210                 215                 220

Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile Gly
225                 230                 235                 240

Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly
                245                 250                 255

Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly
            260                 265                 270

Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn
        275                 280                 285

Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp
    290                 295                 300

Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly
305                 310                 315                 320

Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
                325                 330
```

<210> 7
<211> 585
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Ra35 N-terminus of MTB32A (Ra35FL)

<400> 7
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tccgcgatgg tcgcccaagt ggggccacag gtggtcaaca tcaacaccaa actgggctac 120
aacaacgccg tgggcgccgg gaccggcatc gtcatcgatc ccaacggtgt cgtgctgacc 180
aacaaccacg tgatcgcggg cgccaccgac atcaatgcgt tcagcgtcgg ctccggccaa 240
acctacggcg tcgatgtggt cgggtatgac cgcacccagg atgtcgcggt gctgcagctg 300
cgcggtgccg gtggcctgcc gtcggcggcg atcggtggcg gcgtcgcggt tggtgagccc 360
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gtcgtcgcga tgggcaacag cggtgggcag ggcggaacgc cccgtgcggt gcctggcagg 420
gtggtcgcgc tcggccaaac cgtgcaggcg tcggattcgc tgaccggtgc cgaagagaca 480
ttgaacgggt tgatccagtt cgatgccgcg atccagcccg gtgaggcggg cgggcccgtc 540
gtcaacggcc taggacaggt ggtcggtatg aacacggccg cgtcc 585

<210> 8
<211> 195
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Ra35 N-terminus of MTB32A (Ra35FL)

<400> 8

Ala	Pro	Pro	Ala	Leu	Ser	Gln	Asp	Arg	Phe	Ala	Asp	Phe	Pro	Ala	Leu
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Pro	Leu	Asp	Pro	Ser	Ala	Met	Val	Ala	Gln	Val	Ala	Pro	Gln	Val	Val
		20					25					30			
Asn	Ile	Asn	Thr	Lys	Leu	Gly	Tyr	Asn	Asn	Ala	Val	Gly	Ala	Gly	Thr
	35					40					45				
Gly	Ile	Val	Ile	Asp	Pro	Asn	Gly	Val	Val	Leu	Thr	Asn	Asn	His	Val
50					55					60					
Ile	Ala	Gly	Ala	Thr	Asp	Ile	Asn	Ala	Phe	Ser	Val	Gly	Ser	Gly	Gln
65				70					75					80	
Thr	Tyr	Gly	Val	Asp	Val	Val	Gly	Tyr	Asp	Arg	Thr	Gln	Asp	Val	Ala
			85					90					95		
Val	Leu	Gln	Leu	Arg	Gly	Ala	Gly	Gly	Leu	Pro	Ser	Ala	Ala	Ile	Gly
		100					105					110			
Gly	Gly	Val	Ala	Val	Gly	Glu	Pro	Val	Val	Ala	Met	Gly	Asn	Ser	Gly
	115					120					125				
Gly	Gln	Gly	Gly	Thr	Pro	Arg	Ala	Val	Pro	Gly	Arg	Val	Val	Ala	Leu
130					135					140					
Gly	Gln	Thr	Val	Gln	Ala	Ser	Asp	Ser	Leu	Thr	Gly	Ala	Glu	Glu	Thr
145				150					155					160	
Leu	Asn	Gly	Leu	Ile	Gln	Phe	Asp	Ala	Ala	Ile	Gln	Pro	Gly	Asp	Ser
			165					170					175		
Gly	Gly	Pro	Val	Val	Asn	Gly	Leu	Gly	Gln	Val	Val	Gly	Met	Asn	Thr
		180					185					190			
Ala	Ala	Ser													
	195														

<210> 9
<211> 447
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Ra12 or MTBRa12 C-terminus of MTB32A (Ra35FL)

<400> 9
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cattccgatc gggcaggcga tggcgatcgc gggccagatc cgatcgggtg gggggtcacc 120
caccgttcat atcgggccta ccgccttcct cggcttgggt gttgtcgaca acaacggcaa 180
cggcgcacga gtccaacgcg tggtcgggag cgctccggcg gcaagtctcg gcatctccac 240
cggcgacgtg atcaccgcgg tcgacggcgc tccgatcaac tcggccaccg cgatggcgga 300
cgcgcttaac gggcatcatc ccggtgacgt catctcggtg aactggcaaa ccaagtcggg 360
cggcacgcgt acagggaacg tgacattggc cgagggaccc ccggcctgat ttcgtcgygg 420
ataccacccg ccggccggcc aattgga 447

<210> 10
<211> 132
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Ra 12 or MTBRa12 C-terminus of MTB32A (Ra35FL)

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Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
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Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20 25 30

Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35 40 45

Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50 55 60

Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65 70 75 80

Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85 90 95

Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100 105 110

Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115 120 125

Gly Pro Pro Ala
130

<210> 11
<211> 851
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB39 (TbH9)

<220>
<221> modified_base
<222> (767)
<223> n = g, a, c or t

<400> 11
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ccgggttgct gcggcggcct acgagacggc gtatgggctg acggtgcccc cgccggtgat 120
cgccgagaac cgtgctgaac tgatgattct gatagcgacc aacctcttgg ggcaaaacac 180
cccggcgatc gcggtcaacg aggccgaata cggcgagatg tgggcccaag acgccgccgc 240
gatgtttggc tacgccgcgg cgacggcgac ggcgacggcg acgttgctgc cgttcgagga 300
ggcgccggag atgaccagcg cgggtgggct cctcgagcag gccgccgcgg tcgaggaggc 360
ctccgacacc gccgcggcga accagttgat gaacaatgtg ccccaggcgc tgaaacagtt 420
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ctcgccgcat cggtcgccga tcagcaacat ggtgtcgatg gccaacaacc acatgtcgat 540
gaccaactcg ggtgtgtcga tgaccaacac cttgagctcg atgttgaagg gctttgctcc 600
ggcggcggcc gcccaggccg tgcaaaccgc ggcgcaaaac ggggtccggg cgatgagctc 660
gctgggcagc tcgctgggtt cttcgggtct gggcggtggg gtggccgcca acttgggtcg 720
ggcggcctcg gtacggtatg gtcaccggga tggcggaaaa tatgcanagt ctggtcggcg 780
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gaaacagtta c 851

<210> 12
<211> 263
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB39 (TbH9)

<220>
<221> MOD_RES
<222> (254)
<223> Xaa = any amino acid

<400> 12
Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
1 5 10 15

Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
20 25 30

Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
35 40 45

Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
50 55 60

Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
65 70 75 80

Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
85 90 95

Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
100 105 110

Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
115 120 125

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Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly
    130                 135                 140

Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
145                 150                 155                 160

His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
                165                 170                 175

Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
            180                 185                 190

Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr Ala
        195                 200                 205

Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
    210                 215                 220

Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
225                 230                 235                 240

Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly
                245                 250                 255

Arg Arg Asn Gly Gly Pro Ala
            260
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<210> 13
<211> 3058
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB39 (TbH9FL)

<400> 13

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tgtggctagc aatgccgctg cggcggcccc gacgactggg gtggtgcccc ccgctgccga 180
tgaggtgtcg gcgctgactg cggcgcactt cgccgcacat gcggcgatgt atcagtccgt 240
gagcgctcgg gctgctgcga ttcatgacca gttcgtggcc acccttgcca gcagcgccag 300
ctcgtatgcg gccactgaag tcgccaatgc ggcggcggcc agctaagcca ggaacagtcg 360
gcacgagaaa ccacgagaaa tagggacacg taatggtgga tttcggggcg ttaccaccgg 420
agatcaactc cgcgaggatg tacgccggcc cgggttcggc ctcgctggtg gccgcggctc 480
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ggcccgggca gatgctgggc gggctgccgg tggggcagat gggcgccagg gccggtggtg 1500
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ggcgtgggcg tcgctggtga ccagcgcgac cccggacagg ccgcgggcga ccaggtcgcg 3000
gaagaacgcc agccagccgg ccccgtcctc ggcggaggtg acctggatgc ccaggatc   3058
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<210> 14
<211> 391
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB39 (TbH9FL)

<400> 14

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Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp
             20                  25                  30

Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
         35                  40                  45

Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
     50                  55                  60

Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65                  70                  75                  80

Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
                 85                  90                  95

Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
            100                 105                 110

Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
        115                 120                 125
```

```
Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
    130                 135                 140

Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
145                 150                 155                 160

Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
                165                 170                 175

Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
            180                 185                 190

Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
        195                 200                 205

Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
    210                 215                 220

Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
225                 230                 235                 240

Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
                245                 250                 255

Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
            260                 265                 270

Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
        275                 280                 285

Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
    290                 295                 300

Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
305                 310                 315                 320

Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
                325                 330                 335

Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
            340                 345                 350

Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
        355                 360                 365

Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
    370                 375                 380

Pro His Ser Pro Ala Ala Gly
385                 390
```

<210> 15
<211> 2287
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:tri-fusion protein MTB72F (Ra12-TbH9-Ra35 or MTB32-MTB39 fusion)

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<221> CDS
<222> (42)..(2231)
<223> MTB72F

<220>
<221> modified_base
<222> (30)
<223> n = g, a, c or t

<220>
<221> modified_base
<222> (33)
<223> n = g, a, c or t

<220>
<221> modified_base
<222> (2270)
<223> n = g, a, c or t

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Met His His His His
1 5

cat cac acg gcc gcg tcc gat aac ttc cag ctg tcc cag ggt ggg cag 104
His His Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln
10 15 20

gga ttc gcc att ccg atc ggg cag gcg atg gcg atc gcg ggc cag atc 152
Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile
25 30 35

cga tcg ggt ggg ggg tca ccc acc gtt cat atc ggg cct acc gcc ttc 200
Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe
40 45 50

ctc ggc ttg ggt gtt gtc gac aac aac ggc aac ggc gca cga gtc caa 248
Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln
55 60 65

cgc gtg gtc ggg agc gct ccg gcg gca agt ctc ggc atc tcc acc ggc 296
Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly
70 75 80 85

gac gtg atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg 344
Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala
90 95 100

atg gcg gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg 392
Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val
105 110 115

acc tgg caa acc aag tcg ggc ggc acg cgt aca ggg aac gtg aca ttg 440
Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu
120 125 130

gcc gag gga ccc ccg gcc gaa ttc atg gtg gat ttc ggg gcg tta cca 488
Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp Phe Gly Ala Leu Pro
135 140 145

```
ccg gag atc aac tcc gcg agg atg tac gcc ggc ccg ggt tcg gcc tcg   536
Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser
150                 155                 160                 165

ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt gac ctg ttt   584
Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe
                170                 175                 180

tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg acg gtg ggg   632
Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly
            185                 190                 195

tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg gcc tcg ccg   680
Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro
        200                 205                 210

tat gtg gcg tgg atg agc gtc acc gcg ggg cag gcc gag ctg acc gcc   728
Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala
    215                 220                 225

gcc cag gtc cgg gtt gct gcg gcg gcc tac gag acg gcg tat ggg ctg   776
Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu
230                 235                 240                 245

acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa ctg atg att   824
Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile
                250                 255                 260

ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg atc gcg gtc   872
Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val
            265                 270                 275

aac gag gcc gaa tac ggc gag atg tgg gcc caa gac gcc gcc gcg atg   920
Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met
        280                 285                 290

ttt ggc tac gcc gcg gcg acg gcg acg gcg acg gcg acg ttg ctg ccg   968
Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro
    295                 300                 305

ttc gag gag gcg ccg gag atg acc agc gcg ggt ggg ctc ctc gag cag   1016
Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln
310                 315                 320                 325

gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg gcg aac cag ttg   1064
Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu
                330                 335                 340

atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag ccc acg cag   1112
Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln
            345                 350                 355

ggc acc acg cct tct tcc aag ctg ggt ggc ctg tgg aag acg gtc tcg   1160
Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser
        360                 365                 370

ccg cat cgg tcg ccg atc agc aac atg gtg tcg atg gcc aac aac cac   1208
Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His
    375                 380                 385
```

```
atg tcg atg acc aac tcg ggt gtg tcg atg acc aac acc ttg agc tcg   1256
Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser
390                 395                 400                 405

atg ttg aag ggc ttt gct ccg gcg gcg gcc cgc cag gcc gtg caa acc   1304
Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Arg Gln Ala Val Gln Thr
                410                 415                 420

gcg gcg caa aac ggg gtc cgg gcg atg agc tcg ctg ggc agc tcg ctg   1352
Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu
            425                 430                 435

ggt tct tcg ggt ctg ggc ggt ggg gtg gcc gcc aac ttg ggt cgg gcg   1400
Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala
        440                 445                 450

gcc tcg gtc ggt tcg ttg tcg gtg ccg cag gcc tgg gcc gcg gcc aac   1448
Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn
    455                 460                 465

cag gca gtc acc ccg gcg gcg cgg gcg ctg ccg ctg acc agc ctg acc   1496
Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr
470                 475                 480                 485

agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg ctg ccg gtg   1544
Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val
                490                 495                 500

ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt gtg ctg cgt   1592
Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val Leu Arg
            505                 510                 515

gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gca gcc ggc gat   1640
Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp
        520                 525                 530

atc gcc ccg ccg gcc ttg tcg cag gac cgg ttc gcc gac ttc ccc gcg   1688
Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala
    535                 540                 545

ctg ccc ctc gac ccg tcc gcg atg gtc gcc caa gtg ggg cca cag gtg   1736
Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val
550                 555                 560                 565

gtc aac atc aac acc aaa ctg ggc tac aac aac gcc gtg ggc gcc ggg   1784
Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly
                570                 575                 580

acc ggc atc gtc atc gat ccc aac ggt gtc gtg ctg acc aac aac cac   1832
Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His
            585                 590                 595

gtg atc gcg ggc gcc acc gac atc aat gcg ttc agc gtc ggc tcc ggc   1880
Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly
        600                 605                 610

caa acc tac ggc gtc gat gtg gtc ggg tat gac cgc acc cag gat gtc   1928
Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val
    615                 620                 625
```

```
gcg gtg ctg cag ctg cgc ggt gcc ggt ggc ctg ccg tcg gcg gcg atc   1976
Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile
630                 635                 640                 645

ggt ggc ggc gtc gcg gtt ggt gag ccc gtc gtc gcg atg ggc aac agc   2024
Gly Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser
                650                 655                 660

ggt ggg cag ggc gga acg ccc cgt gcg gtg cct ggc agg gtg gtc gcg   2072
Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala
            665                 670                 675

ctc ggc caa acc gtg cag gcg tcg gat tcg ctg acc ggt gcc gaa gag   2120
Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu
        680                 685                 690

aca ttg aac ggg ttg atc cag ttc gat gcc gcg atc cag ccc ggt gat   2168
Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp
    695                 700                 705

tcg ggc ggg ccc gtc gtc aac ggc cta gga cag gtg gtc ggt atg aac   2216
Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn
710                 715                 720                 725

acg gcc gcg tcc tag gatatccatc acactggcgg ccgctcgagc agatccggnt   2271
Thr Ala Ala Ser

gtaacaaagc ccgaaa                                                 2287
```

<210> 16
<211> 729
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:tri-fusion protein MTB72F (Ra12-TbH9-Ra35 or MTB32-MTB39 fusion)

<400> 16

```
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
  1               5                  10                  15

Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
             20                  25                  30

Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
         35                  40                  45

Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
     50                  55                  60

Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
 65                  70                  75                  80

Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
                 85                  90                  95
```

```
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
            100                 105                 110

Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
        115                 120                 125

Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp
    130                 135                 140

Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly
145                 150                 155                 160

Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val
                165                 170                 175

Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp
            180                 185                 190

Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val
        195                 200                 205

Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln
    210                 215                 220

Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu
225                 230                 235                 240

Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg
                245                 250                 255

Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr
            260                 265                 270

Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln
        275                 280                 285

Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr
    290                 295                 300

Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly
305                 310                 315                 320

Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala
                325                 330                 335

Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu
            340                 345                 350

Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu
        355                 360                 365

Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser
    370                 375                 380

Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr
385                 390                 395                 400

Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Arg
                405                 410                 415
```

```
Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser
            420                 425                 430

Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala
        435                 440                 445

Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala
    450                 455                 460

Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro
465                 470                 475                 480

Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu
                485                 490                 495

Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu
            500                 505                 510

Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
        515                 520                 525

Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe
    530                 535                 540

Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln
545                 550                 555                 560

Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
                565                 570                 575

Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
            580                 585                 590

Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
        595                 600                 605

Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
    610                 615                 620

Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
625                 630                 635                 640

Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val Val
                645                 650                 655

Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro
            660                 665                 670

Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
        675                 680                 685

Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
    690                 695                 700

Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln
705                 710                 715                 720

Val Val Gly Met Asn Thr Ala Ala Ser
                725
```

<210> 17
<211> 2190
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MTB72FMutSA
(Ra12-TbHp-Ra35MutSA) cDNA

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cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat ccgatcgggt 120
gggggtcac ccaccgttca tatcgggcct accgccttcc tcggcttggg tgttgtcgac 180
aacaacggca acggcgcacg agtccaacgc gtggtcggga gcgctccggc ggcaagtctc 240
ggcatctcca ccggcgacgt gatcaccgcg gtcgacggcg ctccgatcaa ctcggccacc 300
gcgatggcgg acgcgcttaa cgggcatcat cccggtgacg tcatctcggt gacctggcaa 360
accaagtcgg gcggcacgcg tacagggaac gtgacattgg ccgagggacc cccggccgaa 420
ttcatggtgg atttcggggc gttaccaccg gagatcaact ccgcgaggat gtacgccggc 480
ccgggttcgg cctcgctggt ggccgcggct cagatgtggg acagcgtggc gagtgacctg 540
ttttcggccg cgtcggcgtt tcagtcggtg gtctggggtc tgacggtggg gtcgtggata 600
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accgcggggc aggccgagct gaccgccgcc caggtccggg ttgctgcggc ggcctacgag 720
acggcgtatg ggctgacggt gcccccgccg gtgatcgccg agaaccgtgc tgaactgatg 780
attctgatag cgaccaacct cttggggcaa aacaccccgg cgatcgcggt caacgaggcc 840
gaatacggcg agatgtgggc ccaagacgcc gccgcgatgt ttggctacgc cgcggcgacg 900
gcgacggcga cggcgacgtt gctgccgttc gaggaggcgc cggagatgac cagcgcgggt 960
gggctcctcg agcaggccgc cgcggtcgag gaggcctccg acaccgccgc ggcgaaccag 1020
ttgatgaaca atgtgcccca ggcgctgcaa cagctggccc agcccacgca gggcaccacg 1080
ccttcttcca agctgggtgg cctgtggaag acggtctcgc cgcatcggtc gccgatcagc 1140
aacatggtgt cgatggccaa caaccacatg tcgatgacca actcgggtgt gtcgatgacc 1200
aacaccttga gctcgatgtt gaagggcttt gctccggcgg cggccgccca ggccgtgcaa 1260
accgcggcgc aaaacggggt ccgggcgatg agctcgctgg gcagctcgct gggttcttcg 1320
ggtctgggcg gtggggtggc cgccaacttg ggtcgggcgg cctcggtcgg ttcgttgtcg 1380
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gtggggccac aggtggtcaa catcaacacc aaactgggct acaacaacgc cgtgggcgcc 1740
gggaccggca tcgtcatcga tcccaacggt gtcgtgctga ccaacaacca cgtgatcgcg 1800
ggcgccaccg acatcaatgc gttcagcgtc ggctccggcc aaacctacgg cgtcgatgtg 1860
gtcgggtatg accgcaccca ggatgtcgcg gtgctgcagc tgcgcggtgc cggtggcctg 1920
ccgtcggcgg cgatcggtgg cggcgtcgcg gttggtgagc ccgtcgtcgc gatgggcaac 1980
agcggtgggc agggcggaac gccccgtgcg gtgcctggca gggtggtcgc gctcggccaa 2040
accgtgcagg cgtcggattc gctgaccggt gccgaagaga cattgaacgg gttgatccag 2100
ttcgatgccg cgatccagcc cggtgatgcg ggcgggcccg tcgtcaacgg cctaggacag 2160
gtggtcggta tgaacacggc cgcgtcctag 2190

<210> 18
<211> 729
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MTB72FMutSA
(Ra12-TbHp-Ra35MutSA)

<400> 18
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15

```
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
            20                  25                  30

Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
        35                  40                  45

Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
    50                  55                  60

Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
65                  70                  75                  80

Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
                85                  90                  95

Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
            100                 105                 110

Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
        115                 120                 125

Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp
    130                 135                 140

Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly
145                 150                 155                 160

Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val
                165                 170                 175

Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp
            180                 185                 190

Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val
        195                 200                 205

Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln
    210                 215                 220

Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu
225                 230                 235                 240

Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg
                245                 250                 255

Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr
            260                 265                 270

Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln
        275                 280                 285

Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr
    290                 295                 300

Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly
305                 310                 315                 320

Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala
                325                 330                 335
```

```
Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu
            340                 345                 350

Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu
        355                 360                 365

Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser
    370                 375                 380

Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr
385                 390                 395                 400

Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala
                405                 410                 415

Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser
            420                 425                 430

Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala
        435                 440                 445

Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala
    450                 455                 460

Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro
465                 470                 475                 480

Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu
                485                 490                 495

Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu
            500                 505                 510

Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
        515                 520                 525

Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe
    530                 535                 540

Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln
545                 550                 555                 560

Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
                565                 570                 575

Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
            580                 585                 590

Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
        595                 600                 605

Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
    610                 615                 620

Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
625                 630                 635                 640

Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val Val
                645                 650                 655
```

```
Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro
           660                 665                 670

Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
        675                 680                 685

Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
    690                 695                 700

Ile Gln Pro Gly Asp Ala Gly Gly Pro Val Val Asn Gly Leu Gly Gln
705                 710                 715                 720

Val Val Gly Met Asn Thr Ala Ala Ser
                725
```

<210> 19
<211> 1797
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:bi-fusion protein TbH9-Ra35 (designated MTB59F)

<220>
<221> CDS
<222> (1)..(1791)
<223> MTB59F

<400> 19

```
cat atg cat cac cat cac cat cac atg gtg gat ttc ggg gcg tta cca   48
His Met His His His His His His Met Val Asp Phe Gly Ala Leu Pro
  1               5                  10                  15

ccg gag atc aac tcc gcg agg atg tac gcc ggc ccg ggt tcg gcc tcg   96
Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser
            20                  25                  30

ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt gac ctg ttt   144
Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe
        35                  40                  45

tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg acg gtg ggg   192
Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly
    50                  55                  60

tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg gcc tcg ccg   240
Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro
65                  70                  75                  80

tat gtg gcg tgg atg agc gtc acc gcg ggg cag gcc gag ctg acc gcc   288
Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala
                85                  90                  95

gcc cag gtc cgg gtt gct gcg gcg gcc tac gag acg gcg tat ggg ctg   336
Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu
            100                 105                 110
```

```
acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa ctg atg att   384
Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile
        115                 120                 125

ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg atc gcg gtc   432
Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val
    130                 135                 140

aac gag gcc gaa tac ggc gag atg tgg gcc caa gac gcc gcc gcg atg   480
Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met
145                 150                 155                 160

ttt ggc tac gcc gcg gcg acg gcg acg gcg acg gcg acg ttg ctg ccg   528
Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro
                165                 170                 175

ttc gag gag gcg ccg gag atg acc agc gcg ggt ggg ctc ctc gag cag   576
Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln
            180                 185                 190

gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg gcg aac cag ttg   624
Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu
        195                 200                 205

atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag ccc acg cag   672
Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln
    210                 215                 220

ggc acc acg cct tct tcc aag ctg ggt ggc ctg tgg aag acg gtc tcg   720
Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser
225                 230                 235                 240

ccg cat cgg tcg ccg atc agc aac atg gtg tcg atg gcc aac aac cac   768
Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His
                245                 250                 255

atg tcg atg acc aac tcg ggt gtg tcg atg acc aac acc ttg agc tcg   816
Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser
            260                 265                 270

atg ttg aag ggc ttt gct ccg gcg gcg gcc gcc cag gcc gtg caa acc   864
Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr
        275                 280                 285

gcg gcg caa aac ggg gtc cgg gcg atg agc tcg ctg ggc agc tcg ctg   912
Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu
    290                 295                 300

ggt tct tcg ggt ctg ggc ggt ggg gtg gcc gcc aac ttg ggt cgg gcg   960
Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala
305                 310                 315                 320

gcc tcg gtc ggt tcg ttg tcg gtg ccg cag gcc tgg gcc gcg gcc aac  1008
Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn
                325                 330                 335

cag gca gtc acc ccg gcg gcg cgg gcg ctg ccg ctg acc agc ctg acc  1056
Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr
            340                 345                 350
```

```
agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg ctg ccg gtg   1104
Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val
        355                 360                 365

ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt gtg ctg cgt   1152
Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val Leu Arg
    370                 375                 380

gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gca gcc ggc gat   1200
Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp
385                 390                 395                 400

atc gcc ccg ccg gcc ttg tcg cag gac cgg ttc gcc gac ttc ccc gcg   1248
Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala
                405                 410                 415

ctg ccc ctc gac ccg tcc gcg atg gtc gcc caa gtg ggg cca cag gtg   1296
Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val
            420                 425                 430

gtc aac atc aac acc aaa ctg ggc tac aac aac gcc gtg ggc gcc ggg   1344
Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly
        435                 440                 445

acc ggc atc gtc atc gat ccc aac ggt gtc gtg ctg acc aac aac cac   1392
Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His
    450                 455                 460

gtg atc gcg ggc gcc acc gac atc aat gcg ttc agc gtc ggc tcc ggc   1440
Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly
465                 470                 475                 480

caa acc tac ggc gtc gat gtg gtc ggg tat gac cgc acc cag gat gtc   1488
Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val
                485                 490                 495

gcg gtg ctg cag ctg cgc ggt gcc ggt ggc ctg ccg tcg gcg gcg atc   1536
Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile
            500                 505                 510

ggt ggc ggc gtc gcg gtt ggt gag ccc gtc gtc gcg atg ggc aac agc   1584
Gly Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser
        515                 520                 525

ggt ggg cag ggc gga acg ccc cgt gcg gtg cct ggc agg gtg gtc gcg   1632
Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala
    530                 535                 540

ctc ggc caa acc gtg cag gcg tcg gat tcg ctg acc ggt gcc gaa gag   1680
Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu
545                 550                 555                 560

aca ttg aac ggg ttg atc cag ttc gat gcc gcg atc cag ccc ggt gat   1728
Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp
                565                 570                 575
```

```
tcg ggc ggg ccc gtc gtc aac ggc cta gga cag gtg gtc ggt atg aac   1776
Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn
            580                 585                 590

acg gcc gcg tcc tag gatatc                                      1797
Thr Ala Ala Ser
        595
```

<210> 20
<211> 596
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:bi-fusion protein TbH9-Ra35 (designated MTB59F)

<400> 20

```
His Met His His His His His His Met Val Asp Phe Gly Ala Leu Pro
  1               5                  10                  15

Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser
             20                  25                  30

Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe
         35                  40                  45

Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly
     50                  55                  60

Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro
 65                  70                  75                  80

Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala
                 85                  90                  95

Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu
            100                 105                 110

Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile
        115                 120                 125

Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val
    130                 135                 140

Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met
145                 150                 155                 160

Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro
                165                 170                 175

Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln
            180                 185                 190

Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu
        195                 200                 205

Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln
    210                 215                 220
```

```
Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser
225                 230                 235                 240

Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His
                245                 250                 255

Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser
            260                 265                 270

Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr
        275                 280                 285

Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu
    290                 295                 300

Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala
305                 310                 315                 320

Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn
                325                 330                 335

Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr
            340                 345                 350

Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val
        355                 360                 365

Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val Leu Arg
    370                 375                 380

Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp
385                 390                 395                 400

Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala
                405                 410                 415

Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val
            420                 425                 430

Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly
        435                 440                 445

Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His
    450                 455                 460

Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly
465                 470                 475                 480

Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val
                485                 490                 495

Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile
            500                 505                 510

Gly Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser
        515                 520                 525

Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala
    530                 535                 540
```

```
Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu
545                 550                 555                 560

Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp
                565                 570                 575

Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn
            580                 585                 590

Thr Ala Ala Ser
        595
```

<210> 21
<211> 500
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB8.4 (DPV) cDNA

<400> 21
cgtggcaatg tcgttgaccg tcggggccgg ggtcgcctcc gcagatcccg tggacgcggt 60
cattaacacc acctgcaatt acgggcaggt agtagctgcg ctcaacgcga cggatccggg 120
ggctgccgca cagttcaacg cctcaccggt ggcgcagtcc tatttgcgca atttcctcgc 180
cgcaccgcca cctcagcgcg ctgccatggc cgcgcaattg caagctgtgc cgggggcggc 240
acagtacatc ggccttgtcg agtcggttgc cggctcctgc aacaactatt aagcccatgc 300
gggccccatc ccgcgacccg gcatcgtcgc cggggctagg ccagattgcc ccgctcctca 360
acgggccgca tcccgcgacc cggcatcgtc gccggggcta ggccagattg ccccgctcct 420
caacgggccg catctcgtgc cgaattcctg cagcccgggg gatccactag ttctagagcg 480
gccgccaccg cggtggagct   500

<210> 22
<211> 96
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB8.4 (DPV)

<400> 22
```
Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
  1               5                  10                  15

Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
             20                  25                  30

Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser
         35                  40                  45

Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
     50                  55                  60

Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
 65                  70                  75                  80

Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
                 85                  90                  95
```

<210> 23
<211> 585
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB9.8 (MSL)

<400> 23
tggattccga tagcggtttc ggcccctcga cgggcgacca cggcgcgcag gcctccgaac 60
gggggccgg gacgctggga ttcgccggga ccgcaaccaa agaacgccgg gtccgggcgg 120
tcgggctgac cgcactggcc ggtgatgagt tcggcaacgg cccccggatg ccgatggtgc 180
cggggacctg ggagcagggc agcaacgagc ccgaggcgcc cgacggatcg gggagagggg 240
gaggcgacgg cttaccgcac gacagcaagt aaccgaattc cgaatcacgt ggacccgtac 300
gggtcgaaag gagagatgtt atgagccttt tggatgctca tatcccacag ttggtggcct 360
cccagtcggc gtttgccgcc aaggcggggc tgatgcggca cacgatcggt caggccgagc 420
aggcggcgat gtcggctcag gcgtttcacc agggggagtc gtcggcggcg tttcaggccg 480
cccatgcccg gtttgtggcg gcggccgcca aagtcaacac cttgttggat gtcgcgcagg 540
cgaatctggg.tgaggccgcc ggtacctatg tggccgccga tgctg 585

<210> 24
<211> 97
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB9.8 (MSL)

<400> 24
Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
1 5 10 15

Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
20 25 30

Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
35 40 45

Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys
50 55 60

Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
65 70 75 80

Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly
85 90 95

Phe

<210> 25
<211> 1742
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB9.9A (MTI, also known as MTI-A)

<220>
<221> modified_base
<222> (1)..(1742)
<223> n = g, a, c or t

<400> 25
ccgctctctt tcaacgtcat aagttcggtg ggccagtcgg ccgcgcgtgc atatggcacc 60
aataacgcgt gtcccatgga tacccggacc gcacgacggt agagcggatc agcgcagccg 120
gtgccgaaca ctaccgcgtc cacgctcagc cctgccgcgt tgcggaagat cgagcccagg 180
ttctcatggt cgttaacgcc ttccaacact gcgacggtgc gcgccccggc gaccacctga 240
gcaacgctcg gctccggcac ccggcgcgcg gctgccaaca ccccacgatt gagatggaag 300
ccgatcaccc gtgccatgac atcagccgac gctcgatagt acggcgcgcc gacaccggcc 360
agatcatcct tgagctcggc cagccggcgg tcggtgccga acagcgccag cggcgtgaac 420
cgtgaggcca gcatgcgctg caccaccagc acaccctcgg cgatcaccaa cgccttgccg 480
gtcggcagat cgggacnacn gtcgatgctg ttcaggtcac ggaaatcgtc gagccgtggg 540
tcgtcgggat cgcagacgtc ctgaacatcg aggccgtcgg ggtgctgggc acaacggcct 600
tcggtcacgg gctttcgtcg accagagcca gcatcagatc ggcggcgctg cgcaggatgt 660
cacgctcgct gcggttcagc gtcgcgagcc gctcagccag ccactcttgc agagagccgt 720
tgctgggatt aattgggaga ggaagacagc atgtcgttcg tgaccacaca gccggaagcc 780
ctggcagctg cggcggcgaa cctacagggt attggcacga caatgaacgc ccagaacgcg 840
gccgcggctg ctccaaccac cggagtagtg cccgcagccg ccgatgaagt atcagcgctg 900
accgcggctc agtttgctgc gcacgcgcag atgtaccaaa cggtcagcgc ccaggccgcg 960
gccattcacg aaatgttcgt gaacacgctg gtggccagtt ctggctcata cgcggccacc 1020
gaggcggcca acgcagccgc tgccggctga acgggctcgc acgaacctgc tgaaggagag 1080
ggggaacatc cggagttctc gggtcagggg ttgcgccagc gcccagccga ttcagntatc 1140
ggcgtccata acagcagacg atctaggcat tcagtactaa ggagacaggc aacatggcct 1200
cacgttttat gacggatccg catgcgatgc gggacatggc gggccgtttt gaggtgcacg 1260
cccagacggt ggaggacgag gctcgccgga tgtgggcgtc cgcgcaaaac atttccggtg 1320
cgggctggag tggcatggcc gaggcgacct cgctagacac catgacctag atgaatcagg 1380
cgtttcgcaa catcgtgaac atgctgcacg gggtgcgtga cgggctggtt cgcgacgcca 1440
acaantacga acagcaagag caggcctccc agcagatcct gagcagntag cgccgaaagc 1500
cacagctgng tacgntttct cacattagga gaacaccaat atgacgatta attaccagtt 1560
cggggacgtc gacgctcatg gcgccatgat ccgcgctcag gcggcgtcgc ttgaggcgga 1620
gcatcaggcc atcgttcgtg atgtgttggc cgcgggtgac ttttggggcg gcgccggttc 1680
ggtggcttgc caggagttca ttacccagtt gggccgtaac ttccaggtga tctacgagca 1740
gg 1742

<210> 26
<211> 2836
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB9.9A (MTI also known as MTI-A)

<220>
<221> modified_base
<222> (104)
<223> n = g, a, c or t

<400> 26
gttgattccg ttcgcggcgc cgccgaagac caccaactcc gctggggtgg tcgcacaggc 60
ggttgcgtcg gtcagctggc cgaatcccaa tgattggtgg ctcngtgcgg ttgctgggct 120
cgattacccc cacggaaagg acgacgatcg ttcgtttgct cggtcagtcg tacttggcga 180
cgggcatggc gcggtttctt acctcgatcg cacagcagct gaccttcggc ccaggggca 240
caacggctgg ctccggcgga gcctggtacc caacgccaca attcgccggc ctgggtgcag 300
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caagttgggc cgtcgcggct ccggccttcg cggagaagcc tgaggcgggc acgccgatgt 420
ccgtcatcgg cgaagcgtcc agctgcggtc agggaggcct gcttcgaggc ataccgctgg 480
cgagagcggg gcggcgtaca ggcgccttcg ctcaccgata cgggttccgc cacagcgtga 540

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cggcgggcgt tgatgccaaa ttgaccgtcc cgacggggct ttatctgcgg caagatttca 720
tccccagccc ggtcggtggg ccgataaata cgctggtcag cgcgactctt ccggctgaat 780
tcgatgctct gggcgcccgc tcgacgccga gtatctcgag tgggccgcaa acccggtcaa 840
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aacgggtggc atcgaaatca acttgttgcg ttgcagtgat ctactctctt gcagagagcc 960
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<210> 27
<211> 94
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB9.9A (MTI, also known as MTI-A) ORF peptide

<400> 27

```
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
  1               5                  10                  15

Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
            20                  25                  30

Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
        35                  40                  45

Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
    50                  55                  60
```

```
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
 65                  70                  75                  80

Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
                 85                  90
```

<210> 28
<211> 1200
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB40 (HTCC#1) cDNA

<400> 28

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accttctggg gattggaata cccaaccaag ggggtatcct ttactcctca ctagagtact 120
tcgaaaaagc cctggaggag ctggcagcag cgtttccggg tgatggctgg ttaggttcgg 180
ccgcggacaa atacgccggc aaaaaccgca accacgtgaa ttttttccag gaactggcag 240
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cgggcgcgat ggccgtagtg ggcggcgcgc ttgcctactt ggtcgtgaaa acgctgatca 480
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cggacatcat ttcggatgtg gcggacatca tcaagggcac cctcggagaa gtgtgggagt 600
tcatcacaaa cgcgctcaac ggcctgaaag agctttggga caagctcacg gggtgggtga 660
ccggactgtt ctctcgaggg tggtcgaacc tggagtcctt ctttgcgggc gtccccggct 720
tgaccggcgc gaccagcggc ttgtcgcaag tgactggctt gttcggtgcg gccggtctgt 780
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```

<210> 29
<211> 392
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB40 (HTCC#1)

<400> 29

```
Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
  1               5                  10                  15

Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
             20                  25                  30

Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
         35                  40                  45

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
     50                  55                  60

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
 65                  70                  75                  80
```

```
Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
                  85                  90                  95

Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
            100                 105                 110

Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
        115                 120                 125

Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
    130                 135                 140

Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
145                 150                 155                 160

Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
                165                 170                 175

Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
            180                 185                 190

Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
        195                 200                 205

Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
    210                 215                 220

Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
225                 230                 235                 240

Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
                245                 250                 255

Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
            260                 265                 270

Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
        275                 280                 285

Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
    290                 295                 300

Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
305                 310                 315                 320

Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
                325                 330                 335

Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
            340                 345                 350

Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
        355                 360                 365

Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
    370                 375                 380

Lys Val Leu Val Arg Asn Val Val
385                 390
```

<210> 30
<211> 1441
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB41 (MTCC#2) cDNA

<400> 30
gaggttgctg gcaatggatt tcgggctttt acctccggaa gtgaattcaa gccgaatgta 60
ttccggtccg gggccggagt cgatgctagc cgccgcggcc gcctgggacg gtgtggccgc 120
ggagttgact tccgccgcgg tctcgtatgg atcggtggtg tcgacgctga tcgttgagcc 180
gtggatgggg ccggcggcgg ccgcgatggc ggccgcggca acgccgtatg tggggtggct 240
ggccgccacg gcggcgctgg cgaaggagac ggccacacag gcgagggcag cggcggaagc 300
gtttgggacg gcgttcgcga tgacggtgcc accatccctc gtcgcggcca accgcagccg 360
gttgatgtcg ctggtcgcgg cgaacattct ggggcaaaac agtgcggcga tcgcggctac 420
ccaggccgag tatgccgaaa tgtgggccca agacgctgcc gtgatgtaca gctatgaggg 480
ggcatctgcg gccgcgtcgg cgttgccgcc gttcactcca cccgtgcaag gcaccggccc 540
ggccgggccc gcggccgcag ccgcggcgac ccaagccgcc ggtgcgggcg ccgttgcgga 600
tgcacaggcg acactggccc agctgccccc ggggatcctg agcgacattc tgtccgcatt 660
ggccgccaac gctgatccgc tgacatcggg actgttgggg atcgcgtcga ccctcaaccc 720
gcaagtcgga tccgctcagc cgatagtgat ccccaccccg ataggggaat tggacgtgat 780
cgcgctctac attgcatcca tcgcgaccgg cagcattgcg ctcgcgatca cgaacacggc 840
cagaccctgg cacatcggcc tatacgggaa cgccggcggg ctgggaccga cgcagggcca 900
tccactgagt tcggcgaccg acgagccgga gccgcactgg ggccccttcg ggggcgcggc 960
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ctggaccacg gccgccccgg agatccagct cgccgttcag gcaacaccca ccttcagctc 1080
cagcgccggc gccgacccga cggccctaaa cgggatgccg gcaggcctgc tcagcgggat 1140
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g 1441

<210> 31
<211> 423
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB41 (MTCC#2)

<400> 31
Met Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr
1 5 10 15

Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Ala Trp Asp
20 25 30

Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
35 40 45

Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala
50 55 60

Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
65 70 75 80

```
Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala
                85                  90                  95

Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala
            100                 105                 110

Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln
        115                 120                 125

Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp
    130                 135                 140

Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala
145                 150                 155                 160

Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro
                165                 170                 175

Ala Gly Pro Ala Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly
            180                 185                 190

Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile
        195                 200                 205

Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr
    210                 215                 220

Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser
225                 230                 235                 240

Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile
                245                 250                 255

Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile
            260                 265                 270

Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
        275                 280                 285

Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu
    290                 295                 300

Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
305                 310                 315                 320

Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
                325                 330                 335

Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro
            340                 345                 350

Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
        355                 360                 365

Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
    370                 375                 380

Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
385                 390                 395                 400
```

Gln Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro
405 410 415

Pro Pro Gly Asn Pro Pro Arg
420

<210> 32
<211> 154
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> ESAT-6

<400> 32
atgacagagc agcagtggaa tttcgcgggt atcgaggccg cggcaagcgc aatccaggga 60
aatgtcacgt ccattcattc cctccttgac gaggggaagc agtccctgac caagctcgca 120
gcggcctggg gcggtagcgg ttcggaagcg tacc 154

<210> 33
<211> 51
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> ESAT-6

<400> 33
Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
1 5 10 15

Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
20 25 30

Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
35 40 45

Glu Ala Tyr
50

<210> 34
<211> 327
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Tb38-1 or 38-1 (MTb11)

<400> 34
cggcacgaga gaccgatgcc gctaccctcg cgcaggaggc aggtaatttc gagcggatct 60
ccggcgacct gaaaacccag atcgaccagg tggagtcgac ggcaggttcg ttgcagggcc 120
agtggcgcgg cgcggcgggg acggccgccc aggccgcggt ggtgcgcttc caagaagcag 180
ccaataagca gaagcaggaa ctcgacgaga tctcgacgaa tattcgtcag gccggcgtcc 240
aatactcgag ggccgacgag gagcagcagc aggcgctgtc ctcgcaaatg ggcttctgac 300
ccgctaatac gaaaagaaac ggagcaa 327

<210> 35
<211> 95
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Tb38-1 or 38-1 (MTb11)

<400> 35
Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
1 5 10 15

Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
20 25 30

Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
35 40 45

Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
50 55 60

Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
65 70 75 80

Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
85 90 95

<210> 36
<211> 542
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> TbRa3

<220>
<221> modified_base
<222> (406)
<223> n = g, a, c or t

<400> 36
gaattcggca cgagaggtga tcgacatcat cgggaccagc cccacatcct gggaacaggc 60
ggcggcggag gcggtccagc gggcgcggga tagcgtcgat gacatccgcg tcgctcgggt 120
cattgagcag gacatggccg tggacagcgc cggcaagatc acctaccgca tcaagctcga 180
agtgtcgttc aagatgaggc cggcgcaacc gcgctagcac gggccggcga gcaagacgca 240
aaatcgcacg gtttgcggtt gattcgtgcg attttgtgtc tgctcgccga ggcctaccag 300
gcgcggccca ggtccgcgtg ctgccgtatc caggcgtgca tcgcgattcc ggcggccacg 360
ccggagttaa tgcttcgcgt cgacccgaac tgggcgatcc gccggngagc tgatcgatga 420
ccgtggccag cccgtcgatg cccgagttgc ccgaggaaac gtgctgccag gccggtagga 480
agcgtccgta ggcggcggtg ctgaccggct ctgcctgcgc cctcagtgcg gccagcgagc 540
gg 542

<210> 37
<211> 66
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> TbRa3

<400> 37
Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala
1 5 10 15

Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val
20 25 30

Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile
35 40 45

Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln
50 55 60

Pro Arg
65

<210> 38
<211> 1993
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> 38 kD

<400> 38
tgttcttcga cggcaggctg gtggaggaag ggcccaccga acagctgttc tcctcgccga 60
agcatgcgga aaccgcccga tacgtcgccg gactgtcggg ggacgtcaag gacgccaagc 120
gcggaaattg aagagcacag aaaggtatgg cgtgaaaatt cgtttgcata cgctgttggc 180
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ggtgacgttg gcggagaccg gtagcacgct gctctacccg ctgttcaacc tgtggggtcc 360
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ccccggcgtg aacctgcccg gcaccgcggt agttccgctg caccgctccg acgggtccgg 720
tgacaccttc ttgttcaccc agtacctgtc caagcaagat cccgagggct ggggcaagtc 780
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ctccggtgat cgctcacaac gctcccgatg tgccggtgct gaactacttg cgcggcgacc 1860
cgggcaacgg ggagggcatg ttggtgtccg gtctggtgtt ggcggtgatg gtcgttccca 1920
ttatcgccac caccactcat gacctgttcc ggcaggtgcc ggtgttgccc cgggagggcg 1980
cgatcgggaa ttc 1993

<210> 39
<211> 374
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> 38 kD

<400> 39
Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
1 5 10 15

Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
20 25 30

Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
35 40 45

Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
50 55 60

Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
65 70 75 80

Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
85 90 95

Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
100 105 110

Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
115 120 125

Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
130 135 140

Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
145 150 155 160

Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
165 170 175

Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
180 185 190

Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
195 200 205

Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
210 215 220

Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
225 230 235 240

Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
245 250 255

Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
260 265 270

```
Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe
        275                 280                 285

Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
    290                 295                 300

Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
305                 310                 315                 320

Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
                325                 330                 335

His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
            340                 345                 350

His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
        355                 360                 365

Ile Ala Thr Ile Ser Ser
    370
```

<210> 40
<211> 999
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> DPEP

<400> 40

```
atgcatcacc atcaccatca catgcatcag gtggacccca acttgacacg tcgcaaggga 60
cgattggcgg cactggctat cgcggcgatg gccagcgcca gcctggtgac cgttgcggtg 120
cccgcgaccg ccaacgccga tccggagcca gcgccccccgg tacccacaac ggccgcctcg 180
ccgccgtcga ccgctgcagc gccacccgca ccggcgacac ctgttgcccc cccaccaccg 240
gccgccgcca acacgccgaa tgcccagccg ggcgatccca acgcagcacc tccgccggcc 300
gacccgaacg caccgccgcc acctgtcatt gccccaaacg caccccaacc tgtccggatc 360
gacaacccgg ttggaggatt cagcttcgcg ctgcctgctg gctgggtgga gtctgacgcc 420
gcccacttcg actacggttc agcactcctc agcaaaacca ccggggaccc gccatttccc 480
ggacagccgc cgccggtggc caatgacacc cgtatcgtgc tcggccggct agaccaaaag 540
ctttacgcca gcgccgaagc caccgactcc aaggccgcgg cccggttggg ctcggacatg 600
ggtgagttct atatgcccta cccgggcacc cggatcaacc aggaaaccgt ctcgctcgac 660
gccaacgggg tgtctggaag cgcgtcgtat tacgaagtca agttcagcga tccgagtaag 720
ccgaacggcc agatctggac gggcgtaatc ggctcgcccg cggcgaacgc accggacgcc 780
gggccccctc agcgctggtt tgtggtatgg ctcgggaccg ccaacaaccc ggtggacaag 840
ggcgcggcca aggcgctggc cgaatcgatc cggcctttgg tcgccccgcc gccggcgccg 900
gcaccggctc ctgcagagcc cgctccggcg ccggcgccgg ccggggaagt cgctcctacc 960
ccgacgacac cgacaccgca gcggacctta ccggcctga                        999
```

<210> 41
<211> 332
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> DPEP

<400> 41

```
Met His His His His His His Met His Gln Val Asp Pro Asn Leu Thr
  1               5                  10                  15
```

```
Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
            20                  25                  30

Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
        35                  40                  45

Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
    50                  55                  60

Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
65                  70                  75                  80

Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
                85                  90                  95

Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
            100                 105                 110

Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
        115                 120                 125

Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
    130                 135                 140

Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
145                 150                 155                 160

Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
                165                 170                 175

Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
            180                 185                 190

Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
        195                 200                 205

Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
    210                 215                 220

Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
225                 230                 235                 240

Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
                245                 250                 255

Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
            260                 265                 270

Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
        275                 280                 285

Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
    290                 295                 300

Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
305                 310                 315                 320

Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
                325                 330
```

<210> 42
<211> 702
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> TbH4

<220>
<221> modified_base
<222> (1)..(702)
<223> n = g, a, c or t

<400> 42
cggcacgagg atcggtaccc cgcggcatcg gcagctgccg attcgccggg tttccccacc 60
cgaggaaagc cgctaccaga tggcgctgcc gaagtagggc gatccgttcg cgatgccggc 120
atgaacgggc ggcatcaaat tagtgcagga acctttcagt ttagcgacga taatggctat 180
agcactaagg aggatgatcc gatatgacgc agtcgcagac cgtgacggtg gatcagcaag 240
agattttgaa cagggccaac gaggtggagg ccccgatggc ggacccaccg actgatgtcc 300
ccatcacacc gtgcgaactc acggnggnta aaaacgccgc ccaacagntg gtnttgtccg 360
ccgacaacat gcgggaatac ctggcggccg gtgccaaaga gcggcagcgt ctggcgacct 420
cgctgcgcaa cgcggccaag gngtatggcg aggttgatga ggaggctgcg accgcgctgg 480
acaacgacgg cgaaggaact gtgcaggcag aatcggccgg ggccgtcgga ggggacagtt 540
cggccgaact aaccgatacg ccgagggtgg ccacggccgg tgaacccaac ttcatggatc 600
tcaaagaagc ggcaaggaag ctcgaaacgg gcgaccaagg cgcatcgctc gcgcactgng 660
gggatgggtg gaacacttnc accctgacgc tgcaaggcga cg 702

<210> 43
<211> 286
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> TbH4

<220>
<221> MOD_RES
<222> (1)..(286)
<223> Xaa = any amino acid

<400> 43
Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val
1 5 10 15

Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln
20 25 30

His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val
35 40 45

Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu
50 55 60

Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe
65 70 75 80

Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu
85 90 95

```
Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala
            100                 105                 110

Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val
        115                 120                 125

Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp
    130                 135                 140

Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn
145                 150                 155                 160

Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg
                165                 170                 175

Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly
            180                 185                 190

Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile
        195                 200                 205

Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe
    210                 215                 220

Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp
225                 230                 235                 240

Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg
                245                 250                 255

Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln
            260                 265                 270

Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Xaa Lys
        275                 280                 285
```

<210> 44
<211> 339
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> DPPD genomic DNA

<400> 44
atgaagttga agtttgctcg cctgagtact gcgatactgg gttgtgcagc ggcgcttgtg 60
tttcctgcct cggttgccag cgcagatcca cctgacccgc atcagccgga catgacgaaa 120
ggctattgcc cgggtggccg atggggtttt ggcgacttgg ccgtgtgcga cggcgagaag 180
taccccgacg gctcgttttg gcaccagtgg atgcaaacgt ggtttaccgg cccacagttt 240
tacttcgatt gtgtcagcgg cggtgagccc ctccccggcc cgccgccacc gggtggttgc 300
ggtggggcaa ttccgtccga gcagcccaac gctccctga 339

<210> 45
<211> 112
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> DPPD

<400> 45
Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala
1 5 10 15

Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp
20 25 30

Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp
35 40 45

Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly
50 55 60

Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe
65 70 75 80

Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro
85 90 95

Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro
100 105 110

<210> 46
<211> 921
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:tri-fusion
protein DPV-MTI-MSL (designated MTb31F) cDNA

<220>
<221> CDS
<222> (1)..(900)
<223> MTb31F

<400> 46
cat atg cat cac cat cac cat cac gat ccc gtg gac gcg gtc att aac 48
His Met His His His His His His Asp Pro Val Asp Ala Val Ile Asn
1 5 10 15

acc acc tgc aat tac ggg cag gta gta gct gcg ctc aac gcg acg gat 96
Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp
20 25 30

ccg ggg gct gcc gca cag ttc aac gcc tca ccg gtg gcg cag tcc tat 144
Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr
35 40 45

ttg cgc aat ttc ctc gcc gca ccg cca cct cag cgc gct gcc atg gcc 192
Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg Ala Ala Met Ala
50 55 60

gcg caa ttg caa gct gtg ccg ggg gcg gca cag tac atc ggc ctt gtc 240
Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val
65 70 75 80

gag tcg gtt gcc ggc tcc tgc aac aac tat gag ctc atg acg att aat 288
Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn
85 90 95

```
tac cag ttc ggg gac gtc gac gct cat ggc gcc atg atc cgc gct cag   336
Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
            100                 105                 110

gcg gcg tcg ctt gag gcg gag cat cag gcc atc gtt cgt gat gtg ttg   384
Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val Leu
        115                 120                 125

gcc gcg ggt gac ttt tgg ggc ggc gcc ggt tcg gtg gct tgc cag gag   432
Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu
    130                 135                 140

ttc att acc cag ttg ggc cgt aac ttc cag gtg atc tac gag cag gcc   480
Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala
145                 150                 155                 160

aac gcc cac ggg cag aag gtg cag gct gcc ggc aac aac atg gcg caa   528
Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln
                165                 170                 175

acc gac agc gcc gtc ggc tcc agc tgg gcc act agt atg agc ctt ttg   576
Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu
            180                 185                 190

gat gct cat atc cca cag ttg gtg gcc tcc cag tcg gcg ttt gcc gcc   624
Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
        195                 200                 205

aag gcg ggg ctg atg cgg cac acg atc ggt cag gcc gag cag gcg gcg   672
Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala
    210                 215                 220

atg tcg gct cag gcg ttt cac cag ggg gag tcg tcg gcg gcg ttt cag   720
Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln
225                 230                 235                 240

gcc gcc cat gcc cgg ttt gtg gcg gcg gcc gcc aaa gtc aac acc ttg   768
Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys Val Asn Thr Leu
                245                 250                 255

ttg gat gtc gcg cag gcg aat ctg ggt gag gcc gcc ggt acc tat gtg   816
Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val
            260                 265                 270

gcc gcc gat gct gcg gcc gcg tcg acc tat acc ggg ttc gat atc cat   864
Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile His
        275                 280                 285

cac act ggc ggc cgc tcg agc aga tcc ggc tgc taa caaagcccga        910
His Thr Gly Gly Arg Ser Ser Arg Ser Gly Cys
    290                 295

aaggaagctg a                                                      921


<210> 47
<211> 299
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence:tri-fusion protein DPV-MTI-MSL (designated MTb31F) cDNA

<400> 47

```
His Met His His His His His His Asp Pro Val Asp Ala Val Ile Asn
  1               5                  10                  15

Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp
             20                  25                  30

Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr
         35                  40                  45

Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg Ala Ala Met Ala
     50                  55                  60

Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val
 65                  70                  75                  80

Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn
                 85                  90                  95

Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
            100                 105                 110

Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val Leu
        115                 120                 125

Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu
    130                 135                 140

Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala
145                 150                 155                 160

Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln
                165                 170                 175

Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu
            180                 185                 190

Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
        195                 200                 205

Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala
    210                 215                 220

Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln
225                 230                 235                 240

Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys Val Asn Thr Leu
                245                 250                 255

Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val
            260                 265                 270

Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile His
        275                 280                 285

His Thr Gly Gly Arg Ser Ser Arg Ser Gly Cys
    290                 295
```

<210> 48
<211> 2168
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:tetra-fusion
protein DPV-MTI-MSL-MTCC#2 (designated MTb71F)

<220>
<221> CDS
<222> (1)..(2133)
<223> MTb71F

<400> 48

```
cat atg cat cac cat cac cat cac gat ccc gtg gac gcg gtc att aac   48
His Met His His His His His His Asp Pro Val Asp Ala Val Ile Asn
  1               5                  10                  15

acc acc tgc aat tac ggg cag gta gta gct gcg ctc aac gcg acg gat   96
Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp
             20                  25                  30

ccg ggg gct gcc gca cag ttc aac gcc tca ccg gtg gcg cag tcc tat  144
Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr
         35                  40                  45

ttg cgc aat ttc ctc gcc gca ccg cca cct cag cgc gct gcc atg gcc  192
Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg Ala Ala Met Ala
     50                  55                  60

gcg caa ttg caa gct gtg ccg ggg gcg gca cag tac atc ggc ctt gtc  240
Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val
 65                  70                  75                  80

gag tcg gtt gcc ggc tcc tgc aac aac tat gag ctc atg acg att aat  288
Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn
                 85                  90                  95

tac cag ttc ggg gac gtc gac gct cat ggc gcc atg atc cgc gct cag  336
Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
            100                 105                 110

gcg gcg tcg ctt gag gcg gag cat cag gcc atc gtt cgt gat gtg ttg  384
Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val Leu
        115                 120                 125

gcc gcg ggt gac ttt tgg ggc ggc gcc ggt tcg gtg gct tgc cag gag  432
Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu
    130                 135                 140

ttc att acc cag ttg ggc cgt aac ttc cag gtg atc tac gag cag gcc  480
Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala
145                 150                 155                 160

aac gcc cac ggg cag aag gtg cag gct gcc ggc aac aac atg gcg caa  528
Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln
                165                 170                 175
```

```
acc gac agc gcc gtc ggc tcc agc tgg gcc act agt atg agc ctt ttg   576
Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu
            180                 185                 190

gat gct cat atc cca cag ttg gtg gcc tcc cag tcg gcg ttt gcc gcc   624
Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
        195                 200                 205

aag gcg ggg ctg atg cgg cac acg atc ggt cag gcc gag cag gcg gcg   672
Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala
    210                 215                 220

atg tcg gct cag gcg ttt cac cag ggg gag tcg tcg gcg gcg ttt cag   720
Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln
225                 230                 235                 240

gcc gcc cat gcc cgg ttt gtg gcg gcg gcc gcc aaa gtc aac acc ttg   768
Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys Val Asn Thr Leu
                245                 250                 255

ttg gat gtc gcg cag gcg aat ctg ggt gag gcc gcc ggt acc tat gtg   816
Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val
            260                 265                 270

gcc gcc gat gct gcg gcc gcg tcg acc tat acc ggg ttc gat atc atg   864
Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile Met
        275                 280                 285

gat ttc ggg ctt tta cct ccg gaa gtg aat tca agc cga atg tat tcc   912
Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr Ser
    290                 295                 300

ggt ccg ggg ccg gag tcg atg cta gcc gcc gcg gcc gcc tgg gac ggt   960
Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Ala Trp Asp Gly
305                 310                 315                 320

gtg gcc gcg gag ttg act tcc gcc gcg gtc tcg tat gga tcg gtg gtg   1008
Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val Val
                325                 330                 335

tcg acg ctg atc gtt gag ccg tgg atg ggg ccg gcg gcg gcc gcg atg   1056
Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala Met
            340                 345                 350

gcg gcc gcg gca acg ccg tat gtg ggg tgg ctg gcc gcc acg gcg gcg   1104
Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala Ala
        355                 360                 365

ctg gcg aag gag acg gcc aca cag gcg agg gca gcg gcg gaa gcg ttt   1152
Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala Phe
    370                 375                 380

ggg acg gcg ttc gcg atg acg gtg cca cca tcc ctc gtc gcg gcc aac   1200
Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala Asn
385                 390                 395                 400

cgc agc cgg ttg atg tcg ctg gtc gcg gcg aac att ctg ggg caa aac   1248
Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln Asn
                405                 410                 415
```

```
agt gcg gcg atc gcg gct acc cag gcc gag tat gcc gaa atg tgg gcc   1296
Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp Ala
            420                 425                 430

caa gac gct gcc gtg atg tac agc tat gag ggg gca tct gcg gcc gcg   1344
Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala Ala
        435                 440                 445

tcg gcg ttg ccg ccg ttc act cca ccc gtg caa ggc acc ggc ccg gcc   1392
Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro Ala
    450                 455                 460

ggg ccc gcg gcc gca gcc gcg gcg acc caa gcc gcc ggt gcg ggc gcc   1440
Gly Pro Ala Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly Ala
465                 470                 475                 480

gtt gcg gat gca cag gcg aca ctg gcc cag ctg ccc ccg ggg atc ctg   1488
Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile Leu
                485                 490                 495

agc gac att ctg tcc gca ttg gcc gcc aac gct gat ccg ctg aca tcg   1536
Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr Ser
            500                 505                 510

gga ctg ttg ggg atc gcg tcg acc ctc aac ccg caa gtc gga tcc gct   1584
Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser Ala
        515                 520                 525

cag ccg ata gtg atc ccc acc ccg ata ggg gaa ttg gac gtg atc gcg   1632
Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile Ala
    530                 535                 540

ctc tac att gca tcc atc gcg acc ggc agc att gcg ctc gcg atc acg   1680
Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile Thr
545                 550                 555                 560

aac acg gcc aga ccc tgg cac atc ggc cta tac ggg aac gcc ggc ggg   1728
Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly Gly
                565                 570                 575

ctg gga ccg acg cag ggc cat cca ctg agt tcg gcg acc gac gag ccg   1776
Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu Pro
            580                 585                 590

gag ccg cac tgg ggc ccc ttc ggg ggc gcg gcg ccg gtg tcc gcg ggc   1824
Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala Gly
        595                 600                 605

gtc ggc cac gca gca tta gtc gga gcg ttg tcg gtg ccg cac agc tgg   1872
Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser Trp
    610                 615                 620

acc acg gcc gcc ccg gag atc cag ctc gcc gtt cag gca aca ccc acc   1920
Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro Thr
625                 630                 635                 640

ttc agc tcc agc gcc ggc gcc gac ccg acg gcc cta aac ggg atg ccg   1968
Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met Pro
                645                 650                 655
```

```
gca ggc ctg ctc agc ggg atg gct ttg gcg agc ctg gcc gca cgc ggc   2016
Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg Gly
            660                 665                 670

acg acg ggc ggt ggc ggc acc cgt agc ggc acc agc act gac ggc caa   2064
Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly Gln
        675                 680                 685

gag gac ggc cgc aaa ccc ccg gta gtt gtg att aga gag cag ccg ccg   2112
Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro Pro
    690                 695                 700

ccc gga aac ccc ccg cgg taa gatttctaaa tccatcacac tggcggccgc      2163
Pro Gly Asn Pro Pro Arg
705                 710

tcgag                                                             2168
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<210> 49
<211> 710
<212> PRT
<213> Artificial Sequence

<220>
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Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp
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Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr
         35                  40                  45

Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg Ala Ala Met Ala
     50                  55                  60

Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val
 65                  70                  75                  80

Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn
                 85                  90                  95

Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
            100                 105                 110

Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val Leu
        115                 120                 125

Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu
    130                 135                 140

Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala
145                 150                 155                 160

Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln
                165                 170                 175
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Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu
180 185 190

Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
195 200 205

Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala
210 215 220

Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln
225 230 235 240

Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys Val Asn Thr Leu
245 250 255

Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val
260 265 270

Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile Met
275 280 285

Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr Ser
290 295 300

Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Ala Trp Asp Gly
305 310 315 320

Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val Val
325 330 335

Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala Met
340 345 350

Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala Ala
355 360 365

Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala Phe
370 375 380

Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala Asn
385 390 395 400

Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln Asn
405 410 415

Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp Ala
420 425 430

Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala Ala
435 440 445

Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro Ala
450 455 460

Gly Pro Ala Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly Ala
465 470 475 480

Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile Leu
485 490 495

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Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr Ser
            500                 505                 510

Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser Ala
        515                 520                 525

Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile Ala
    530                 535                 540

Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile Thr
545                 550                 555                 560

Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly Gly
                565                 570                 575

Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu Pro
            580                 585                 590

Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala Gly
        595                 600                 605

Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser Trp
    610                 615                 620

Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro Thr
625                 630                 635                 640

Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met Pro
                645                 650                 655

Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg Gly
            660                 665                 670

Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly Gln
        675                 680                 685

Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro Pro
    690                 695                 700

Pro Gly Asn Pro Pro Arg
705                 710
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<210> 50
<211> 588
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Ra35 N-terminus of MTB32A (Ra35FL)

<400> 50
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aacaacgccg tgggcgccgg gaccggcatc gtcatcgatc ccaacggtgt cgtgctgacc 180
aacaaccacg tgatcgcggg cgccaccgac atcaatgcgt tcagcgtcgg ctccggccaa 240
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cgcggtgccg gtggcctgcc gtcggcggcg atcggtggcg gcgtcgcggt tggtgagccc 360
gtcgtcgcga tgggcaacag cggtgggcag ggcggaacgc cccgtgcggt gcctggcagg 420
gtggtcgcgc tcggccaaac cgtgcaggcg tcggattcgc tgaccggtgc cgaagagaca 480
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ttgaacgggt tgatccagtt cgatgccgcg atccagcccg gtgaggcggg cgggcccgtc 540
gtcaacggcc taggacaggt ggtcggtatg aacacggccg cgtcctag              588
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